REMARKS

Applicants gratefully acknowledge the withdrawal of rejections and objections not set forth in the Office Action of June 7, 2005.

Claims 20-21, 62-67, 69, 71-74, 76-78 and 80-82 are pending and stand rejected.

Applicant thanks the Examiner for the courtesy of a personal interview on October 20, 2005. The rejections under §§ 112 and 102(b) were discussed during the interview, including the designation "Met1," enablement and written description for full and partial Arabidopsis sequences, and differences between the cited art and the claims as amended herein. Applicant respectfully requests reconsideration and allowance in view of the amendments and remarks in this Response.

Specification

The specification has been amended at page 10, line 29 to correct the date of publication of the Finnegan et al. article to conform to the proper date of publication, shown elsewhere in the specification at page 11, line 2 and page 42, line 15.

The specification has been amended at page 18, line 17 to correct typographical errors in the accession number. Both the Finnegan et al. and Ronemus et al. references cited at page 10, line 27 to page 11, line 4, refer to the Arabidopsis DNA methyltransferase sequence that was deposited in 1993 under Genbank number L10692. Furthermore, a BlastN search using the primer sequences in Example 3 of the specification, designated SEQ ID NOS: 5 and 6, identify Genbank entry L10692. Therefore, it is apparent that L10692 was intended rather than C10692.

Table 1 has been amended to correct formatting errors and to conform the left-hand column of the Table to the specification. Specifically, the left-hand column of Table 1 has been amended at rows 11 and 13 to reflect the proper notation for the indicated cross. The data for a 2xmet-2x cross are found in the specification at page 25, lines 10-14, and also provided in row 12 of Table 1. The data for a 2x-2xmet cross are found in the specification at page 25, lines 16-20, and also provided in row 10. Footnote 8 indicates that the data in rows 11 and 13 was

obtained from a subsequent experiment. Thus, the cross shown in rows 10-11 is a 2x-2xmet cross, and the cross shown in rows 12-13 is a 2xmet-2x cross. Table 1 has been amended at rows 11 and 13 to indicate the proper notation and to conform the Table to the specification.

The left-hand column of Table 1 has also been amended at rows 8-9 to reflect the proper notation for the indicated crosses. A 2xmet-2xmet cross was used for comparison purposes, as indicated at page 25, lines 14-16 and 17-20. The results of the cross shown in row 8 have the number of peripheral endosperm nuclei, chalazal endosperm volume and seed weight that match the percentage differences indicated at page 25. Thus, row 8 is the 2xmet-2xmet cross used for comparison. Footnote 8 indicates that the data in row 9 was obtained from a subsequent experiment. Therefore, the cross shown in rows 8-9 is a 2xmet-2xmet cross, and the left-hand column of Table 1 has been amended at rows 8-9 to reflect the proper notation.

Footnote 8 of Table 1 has been amended to correct typographical errors and for grammatical clarity.

The left-hand column of Table 3 at page 34 has been amended to correct a typographical error and conform Table 3 to the specification at page 34, lines 10-21. The specification indicates that a cross of 4x *A. thaliana* by *C. arenosa* results in 100% plump seed that germinates at high frequency. See specification at page 34, lines 10-11. These statements correspond to the second row of Table 3 at page 34. The specification indicates that a cross of diploid *A. thaliana* by *C. arenosa* results in 100% shrivelled seed that fails to germinate. See specification at page 34, lines 13-15. These statements correspond to the third row of Table 3 at page 34. Thus, it is apparent that the third row of the left-hand column of Table 3 should indicate that a cross of 2x *A. thaliana* by *C. arenosa* was carried out.

The specification at page 34, line 26, has been amended to refer to Table 4 rather than Table 3. The sentence at page 34, lines 25-26 refers to *Arabidopsis* plants heterozygous for the *fie-1* mutation. The data in Table 4 clearly relate to heterozygous *fie-1* plants, in contrast to the data Table 3, which relate to interspecific hybridization.

Table 4 at page 37 has been amended to insert a parenthesis mark in the header for "Seed weight."

Claims

The claim amendments presented above amend claims 20, 62, 66, 69, 77 and 80, and cancel claims 72-74. New claims 83-93 are presented.

Claims 20 and 62 have been amended to recite a promoter that targets expression to female germ line cells. Claims 20 and 62 have also been amended to recite a full or partial *Arabidopsis* DNA methyltransferase 1 (Met1) sequence. Support for the amendments to claims 20 and 62 can be found throughout the specification, e.g., page 10, line 27 to page 11, line 4 and page 15, lines 2-4. Claim 77 has been amended to conform the claim language to that of claim 20, from which claim 77 depends.

Claims 72-74 have been cancelled without prejudice.

Claims 66 and 80 have been amended to conform the language to that of claim 20, from which these claims directly or indirectly depend. Claim 69 has been amended to conform the language to that of claim 62, from which this claim depends.

Support for new claims 83-93 can be found, e.g., at page 15, lines 2-4, page 29, lines 14-15 and page 32, lines 6-8.

Claims 20-21, 62-67, 69, 71, 76-78 and 80-93 are pending upon entry of the above amendments.

Rejections Under 35 U.S.C. § 112

Indefiniteness

The Examiner rejected claims 20-21, 62-67, 69, 71-74, 76-78, and 80-82 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention. The designation of a nucleic acid sequence by "Met1" was considered to be arbitrary and to create ambiguity in the claims. It was contended that the Applicant had not explicitly defined "Met1" to denote a specific nucleic acid sequence.

Applicant respectfully disagrees with respect to the amended claims for reasons of record and the following reasons. The instant specification describes Met1 as a DNA methyltransferase from *Arabidopsis*. See specification at page 10, line 27 to page 11, line 4, where it is stated that:

> *Arabidopsis* plants expressing a DNA methyltransferase 1 (Met1) antisense (Met1as) gene contain reduced levels of DNA methyltransferase activity and a correspondingly reduced level of general DNA methylation (Finnegan et al, 1995; Ronemus et al., 1996).

The Finnegan *et al.* reference cited in this sentence is Finnegan et al., Proc. Natl. Acad. Sci. USA 93: pp. 8449–8454 (1996) (hereinafter "Finnegan 2").

The Finnegan 2 reference states at page 8449, left-hand column that:

> The isolation of a cDNA encoding a putative DNA methyltransferase (MET1) of Arabidopsis (7) has enabled us to investigate the role of DNA methylation in plant development using a reverse genetics approach.

Reference (7) in this sentence is Finnegan, et al., Nucleic Acids Res. 21: 2383-2388 (1993), (hereinafter "Finnegan 1"). The Finnegan 1 reference states at page 2385, right-hand column that:

> The length of the methyltransferase cDNA assembled from the overlapping cDNA clones Yc8 and Yc2 is 4720bp not including a poly A tail (Accession No. L10692), which agrees with the estimate based on Northern analysis of 4.7kb (data not shown).

Thus, it would have been apparent to one of ordinary skill that the authors of Finnegan 1 cloned and sequenced a methyltransferase from *Arabidopsis* and published their results in 1993. The nucleotide sequence was deposited as Accession No. L10692. The authors of Finnegan 2 designated their cloned cDNA corresponding to this accession number as "MET1." See Finnegan 2 at page 8449, left-hand column, last paragraph.

The Ronemus et al. reference cited in the instant specification refers to MET1 as a DNA methyltransferase from *Arabidopsis*, and cites the Finnegan 1 article. Ronemus et al. at page 654, left-hand column, last paragraph. The authors of Ronemus et al. also designated their 4.3 kb cDNA as a "MET1 cDNA." See Ronemus at page 654, Figure 1.

The present specification refers to a DNA methyltransferase 1 (Met1) and cites Finnegan 2 and Ronemus et al. Therefore, Applicant respectfully submits that one of skill in the art would recognize that "*Arabidopsis* DNA methyltransferase (Met1) sequence" is not arbitrary, not ambiguous, and is clearly defined. It is a designation for the sequence shown in Accession No.

L10692, the same sequence referred to by Finnegan 2 and Ronemus et al. One of ordinary skill, upon reading the present specification, including page 10, line 27 to page 11, line 4, would have comprehended that pending claim 20 refers to the sequence in Accession No. L10692.

The Examiner has raised the possibility that the sequence could be designated by some other arbitrary means, or the assignment of the name could be arbitrarily changed to designate a different nucleic acid sequence. It is true there is no guarantee that abbreviations for genes and nucleotide sequences will remain the same. However, the present specification will always refer to Ronemus et al. and Finnegan 2. Finnegan 2 will always refer to Finnegan 1. Finnegan 1 will always refer to Accession No. L10692. Accession No. L10692 as of 1993 will always contain the *Arabidopsis* Met1 sequence cloned by Finnegan 1. Therefore, the designation *Arabidopsis* Met1 sequence will always refer to the sequence of Accession No. L10692, despite any future hypothetical changes in abbreviation.

The Examiner is requested to withdraw the rejection of claims 20-21, 62-67, 69, 71, 76-78 and 80-82 under 35 U.S.C. § 112, second paragraph.

Written Description

The Examiner rejected claims 20-21, 62-67, 69, 71-74, 76-78, and 80-82 under 35 U.S.C. §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicant respectfully disagrees at least for reasons of record and the following reasons.

The Examiner contended that the claims relate to a genus of sequences. The Examiner is correct. The Examiner also contended that the Applicant has not disclosed a representative number of sequences identified by SEQ ID NO or any partial sequences that have the same function as the full length sequence. Applicant respectfully submit that the specification satisfies the written description requirement.

Compliance with § 112 requires sufficient information in the specification to show that the inventor possessed the invention at the time of that original disclosure. See Vas-Cath, 935

F.2d at 1563-64 ("[T]he applicant must . . . convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention."); Union Oil Co. of Cal. v. Atl. Richfield Co., 208 F.3d 989, 997 (Fed. Cir. 2000) ("The written description requirement does not require the applicant 'to describe exactly the subject matter claimed, [instead] the description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed.'" (citation omitted)). The written description requirement may be satisfied "if in the knowledge of the art the disclosed function is sufficiently correlated to particular, known structure." Amgen Inc. v. Hoechst Marion Roussel, Inc., 314 F.3d 1313, 1332 (Fed. Cir. 2002).

The Court of Appeals for the Federal Circuit (CAFC) has recognized that disclosure of specific sequences is not a *per se* requirement for satisfying written description. For example, in Capon v. Dudas, the Court stated that "[w]hen the prior art includes the nucleotide information, precedent does not set a *per se* rule that the information must be determined afresh." Capon v. Eshhar v. Dudas, 03-1480, 1481 at 15 (Fed. Cir. Aug. 12, 2005). The claims at issue in Capon recited, *inter alia,* "a first gene segment encoding a single-chain Fv domain (scFv) of a specific antibody . . ." and "DNA encoding a non-MHC restricted extracellular binding domain which is obtained from a single chain antibody that binds specifically to at least one ligand . . .." Id. at pages 5 and 7. The CAFC held that "the Board erred in ruling that §112 imposes a *per se* rule requiring recitation in the specification of the nucleotide sequence of claimed DNA, when that sequence is already known in the field." Id. at page 20. A copy of Capon is attached hereto.

One of ordinary skill would have clearly recognized from the instant specification that Applicant was in possession of the claimed invention. The instant specification states in the context of decreasing the degree of methylation that "one can use antisense sequences, e.g., the Met1as "gene". In addition, it has been found that incorporation of whole or partial copies of an already present gene can result in suppression of gene expression." See, specification at page 18, lines 23-30. The specification indicates that the nucleotide sequences for *Arabidopsis* and *Z. mays* MET1 were known in the field. See, e.g., specification at page 32, lines 6-8 and lines 27-29. The specification indicates that "[e]xpression of the MET1 gene can be reduced in the

female or male germ lines by employing techniques known in the art. For example MET1 down-regulation can be achieved by expressing antisense MET1 or antisense MET1 fragments or sense MET1 or partial sense MET1 or ribozymes directed against MET1 or combinations of the preceding, from promoters expressed in the required germ-line. Below is an example of an antisense MET1 approach." See, specification at page 30, lines 15-19. The specification (Examples 3-4) goes on to describe the construction of an antisense MET1 construct targeted to the female germ line and its use to produce modified endosperm. See, specification at page 32, lines 1-28. In view of the clear description in the specification, and the construction and use of a partial sequence for downregulating MET1, one of ordinary skill would have clearly recognized that the Applicant understood and had invented what is now claimed.

The Examiner is requested to withdraw the rejection of claims 20-21, 62-67, 69, 71, 76-78 and 80-82 under 35 U.S.C. §112, first paragraph.

Scope of Enablement

The Examiner rejected claims 20-21, 62-67, 69, 71-74, 76-78, and 80-82 under 35 U.S.C. § 112, first paragraph, asserting that the specification, while being enabling for a method for increasing the amount of endosperm in a seed comprising a construct comprising the MET1 cDNA of Example 3, did not reasonably provide enablement for the pending claims. The Examiner asserted that the specification does not provide guidance for partial sequences of Arabidopsis or Z. mays MET1, and that undue trial and error would be required by one of skill in the art.

Applicant traverses with respect to the claims as amended. The references cited by the Examiner do not demonstrate non-enablement of the pending claims, but in fact support enablement. These references demonstrate a high level of skill in the art for down regulation technologies such as antisense and cosuppression, and that those of ordinary skill knew how to make and use sequences for downregulation. The references demonstrate that use of these technologies required, at most, routine experimentation. Courts have noted that in fields such as this, where the art typically engages in experimentation, even complex experimentation is not

necessarily undue. See, e.g., In re Certain Limited-Charge Cell Culture Microcarriers 221 USPQ 1165, 1174 (Int'l Trade Comm'n 1983), aff'd. sub nom., Massachusetts Institute of Technology v. A.B. Fortia, 774 F.2d 1104, 227 USPQ 428 (Fed. Cir. 1985). Applicant will discuss each of the references applied by the Examiner in turn.

Jacobsen et al. (Jacobsen)

The Examiner asserted that Jacobsen teaches unpredictability using the claimed method, because the reference reports that the Superman gene was found to be hypermethylated in a MET1 antisense plant instead of hypomethylated, as is the outcome in Applicant's method.

The Jacobsen reference reports that the Superman gene was hypermethylated in a MET1 antisense *Arabidopsis* line. Jacobsen, at page 180, left-hand column. However, the present invention relates to downregulation of DNA methylating enzymes present in plants and the degree of DNA methylation of nucleic acid in plants. It does not specifically relate to the Superman gene or any other particular gene. That is, the outcome in Applicant's method is not hypomethylation of the Superman gene, but is a reduction in the degree of DNA methylation of nucleic acid in the plant.

There is no logical reason why the data reported in Jacobsen about a particular gene would lead one of ordinary skill to conclude that claims about downregulation of DNA methylating enzymes would not have been enabled because antisense MET1 constructs have been uniformly successful in reducing the degree of DNA methylation in a plant. U.S. Patent 6,011,200 describes the use of a Met1 antisense construct that was ~4,300 nucleotides in length. This construct was successful in reducing the degree of DNA methylation. See, Example 1 of U.S. Patent 6,011,200, in particular column 13, lines 18-23. Finnegan 2 describe the use of an antisense MET1 construct that was ~2550 nucleotides in length. This construct was successful in reducing the degree of DNA methylation. Finnegan et al. Proc. Natl. Acad. Sci. USA 93:8449 (1996), at page 8450, Table 1. Jacobsen reports that an antisense MET1 construct was successful in reducing the degree of DNA methylation in a plant by 80-90%. Jacobsen at page 180, left-hand column.

In fact, the Examiner has not pointed to a single instance where downregulation of a MET1 gene failed to reduce the degree of methylation. U.S. Patent 6,011,200, Finnegan et al. and Jacobsen, although recognizing that downregulation of MET1 reduced the degree of methylation, did not recognize the importance of a female germ line promoter. Applicant did. Nevertheless, it is apparent that one of ordinary skill, with knowledge of the general principles of antisense and the present specification at hand, would have appreciated that antisense procedures could be readily employed to practice the claimed invention. Data regarding methylation of the Superman gene has no relevance to the pending claims and certainly does not contradict the experimental evidence that MET1 antisense constructs are successful in reducing DNA methylation. The present Office Action provides no explanation as to why data reported in Jacobsen would have been considered to contradict such evidence.

The Examiner asserted that cloning methods such as hybridization or PCR are not the issue with respect to enablement. Office Action at page 7, lines 1-4. The Examiner asserted that Applicant has not disclosed which sequences can be used in the claimed method and that undue experimentation would be required to identify, isolate and test the multitude of non-exemplified sequences.

Applicant submits that methods are the issue, because any experimentation required by one of ordinary skill would have utilized routine methods. Applicants believe the Examiner would acknowledge that PCR cloning and chemical synthesis of DNA was routine as of the earliest priority date of the present application. In view of the known methods available for cloning and/or synthesizing DNA, Applicants submit that one of ordinary skill could have readily identified and isolated any and all non-exemplified *Arabidopsis* and *Z. mays* MET1 sequences. Therefore, the only question is whether testing non-exemplified sequences would have been routine for one of ordinary skill.

Based on guidance in the instant application and knowledge in the art, testing non-exemplified sequences would have been routine. First, the working examples give detailed instructions on how to test sequences for their effect on endosperm. Second, the general principles of downregulation technologies would have been well known to one of ordinary skill.

In the case of antisense technology, see, e.g., U.S. 6,940,001, U.S. 6,900,368, U.S. 6,897,359, U.S. 6,455,688, U.S. 6,355,862 and U.S. 6,329,567. It would have been known to one of ordinary skill that antisense constructs complementary to at least a portion of the messenger RNA for MET1 can be constructed that hybridize with the corresponding mRNA and interfere with expression. See van der Krol et al., Biotechniques 6:958-976(1988). Antisense inhibition has been shown using either full-length or partial cDNA. See, e.g., Sheehy et al., Proc. Natl. Acad. Sci. USA 85:8805-8809 (1988); Cannon et al., Plant Mol. Biol. 15:39-47 (1990). One of ordinary skill would have also known that 3′ non-coding sequences (Ch'ng et al., Proc. Natl. Acad. Sci. USA (1989) 86:10006-10010) and fragments of 5′ coding sequence, (Cannon et al., Plant Mol. Biol. (1990) 15:39-47), can be used. Copies of these references are in the attached IDS.

Fourgoux-Nicol

The Examiner asserted that Fourgoux-Nicol teaches the unpredictability of hybridization techniques and that the claimed methods encompass degenerate primers. Applicant respectfully disagrees.

The pending claims do not encompass degenerate primers. For example, pending claim 20 is directed to a "method for the production of modified endosperm, which comprises the step of introducing a nucleic acid molecule into a plant, the nucleic acid molecule comprising a promoter that drives expression that is restricted to female germ line cells and a sequence whose transcription product comprises a partial or full-length Arabidopsis Met1 sequence, wherein the introduced nucleic acid is effective for down-regulating one or more DNA methylating enzymes present in the plant, whereby the degree of DNA methylation of nucleic acid in the plant is reduced as compared to a control plant." Applicants respectfully submit that there are no words or phrases in the pending claims that would encompass a degenerate primer.

Gutterson et al. (Gutterson)

The Examiner asserted that although Gutterson may teach enablement for some aspects of co-suppression, the reference also teaches "unpredictability" of co-suppression.

Gutterson states that "[a]lthough heterologous sequences can be used for sense suppression, a high degree of sequence identity was needed" for a chalcone synthase gene. Gutterson at page 965, left-hand column. Here, MET1 sequences have a high degree of sequence identity. The attached diagram shows an alignment of DNA methyltransferase sequences from *Arabidopsis* and *Zea mays*. The overall nucleotide sequence identity between the *Arabidopsis* and *Zea* sequences is about 64%. Moreover, there a numerous regions in these sequences that have greater than 75% identity. See, e.g., nucleotides 731 to 856 (76% identity), nucleotides 3329 to 3981 (82% identity), 3635 to 3720 (91% identity), and nucleotides 4331 to 4590 (82% identity). These are strikingly high percent identities given that *Arabidopsis* is a dicot and *Zea* is a monocot. The AtMET1 and ZmMET1 nucleotide sequences even have about 58% identity to the mouse DNA methyltransferase, Dnmt1 (data not shown).

The principles of cosuppression would have been well known to one of ordinary skill in the art. See, e.g., U.S. 6,255,561, U.S. 6,429,356 and U.S. 6,459,019. See also, Jorgensen, Trends Biotechnol. 8:340-344 (1990); Niebel et al., Curr. Top. Microbiol. Immunol. 197:91-103 (1995); Flavell et al. Curr. Top. Microbiol. Immunol. 197:43-56(1995); Palaqui and Vaucheret, Plant. Mol. Biol. 29:149-159 (1995); Vaucheret et al.. Mol. Gen. Genet. 248;311-317 (1995); de Borne et al., Mol. Gen. Genet. 243:613-621(1994); Hamilton et al. Plant J. 15: 737-746 (1998) and Taylor, Plant Cell 9:1245-1249 (1997). Copies of these references are included in the attached IDS.

Thus, the state of the art as a whole does not teach that cosuppression is "unpredictable," but instead provides guidance to one of ordinary skill in its use. One of ordinary skill in the art, with knowledge of the general principles of cosuppression and the present specification at hand, would have had the guidance provided by Gutterson, along with the guidance provided by Jorgensen, Niebel et al., Flavell et al., Palaqui and Vaucheret, Vaucheret et al., de Borne et al.,

Hamilton et al., and Taylor. One of ordinary skill would have used that guidance in order to practice the present invention, and could have done so with only routine experimentation.

Emery et al. (Emery)

Emery was published in 2003, about 4 years after the priority date of the present application. Enablement is to be determined as of the priority date. According to MPEP §2164.05(a), post filing-date references can only be used "if individuals of skill in the art state that a particular invention is not possible years after the filing date...." Applicant can find no statement in Emery that the particular invention recited in the pending claims is not possible. Therefore, Emery is not relevant to enablement of the present claims.

Mazzolini et al. (Mazzolini)

The Examiner cited In re Wright for the proposition that the fact that a reference (Mazzolini) is old is not impressive absent a showing that the art tried and failed to solve the same problem notwithstanding its presumed knowledge of the references. In re Wright, 569 F.2d 1124, 193 USPQ 332 (CCPA 1977). However, the issue in Wright was obviousness, whereas Mazzolini was cited with respect to an enablement rejection. A copy of Wright is enclosed herewith.

Here, the Office Action has no showing that the art tried and failed to solve the same problem after the publication of Mazzolini. In contrast, Applicants presented evidence that by 1999 the state of the art of ribozyme technology in plants had advanced beyond Mazzolini. See Response filed February 25, 2005, at page 16.

As stated in the Manual of Patent Examining Procedure, "[t]he state of the art for a given technology is not static in time. It is entirely possible that a disclosure filed on January 2, 1990, would not have been enabled. However, if the same disclosure had been filed on January 2, 1996, it might have enabled the claims. Therefore, the state of the prior art must be evaluated for each application based on its filing date." MPEP § 2164.05(a). In other words, the MPEP recognizes that the state of the art changes with time, and that the age of a reference does have an

impact on enablement. Age is relevant because subsequent advances in technology can make data and/or conclusions in the reference outdated.

Applicant requests that the rejection be withdrawn with respect to claims 20-21, 62-67, 69, 71, 76-78 and 80-82 under 35 U.S.C. §112, first paragraph.

Rejection under 35 USC § 102(b)

The Examiner rejected claims 20-21, 64-65, 77-78 and 81 under 35 U.S.C. § 102(b) as being anticipated by Ronemus et al (1996, Science 273:654-657). This rejection was maintained for the reasons of record set forth in the Official action mailed October 25, 2004. The Examiner asserted that, with respect to the term "directing expression in female germ line cells," the Applicant was arguing limitations that are not stated in the claims. The Examiner cited Van Geuns for the proposition that limitations from the specification are not read into the claims. In re Van Geuns, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

Applicant respectfully disagrees for the reasons set forth in the Response filed February 25, 2005. The Examiner is correct that limitations from the specification are not read into the claims. However, the Patent and Trademark Office is expected to interpret limitations in the claims in light of the ordinary and customary meanings attributed to them by those of ordinary skill in the art. See, e.g., Brookhill-Wilk 1, LLC v. Intuitive Surgical, Inc., 334 F.3d 1294, 1298, 67 USPQ2d 1132, 1136 (Fed. Cir. 2003). Here, the specification specifically differentiates expression targeted to female germ line cells from the expression that occurs with a CaMV35S-regulated *MET1* antisense construct.

At page 15, lines 1-5, it is stated that

> "The present invention further provides methods for removing or attenuating genomic imprinting, based on targeting the germ line or gametes with transgenes which alter the methylation pattern of genes, or their capacity to form or maintain imprints, within the developing endosperm."

See also, specification at page 15, lines 12-26, where it is stated that:

> [t]he restriction of imprint removal or attenuation to one or other sex of gamete is desirable for 3 reasons:
>
> 1. To provide for removal of imprinting in a single sex of gamete within an individual plant. This will produce the asymmetry of imprinting that is required to mimic the interploidy cross effect in a self-fertilizing plant.

2. To prevent developmental abnormalities that are associated with generalized hypomethylation, such as occurs with the CaMV35S driven Met1 antisense gene.

3. To prevent the attenuation of the interploidy cross effect due to the expression of the hypomethylation gene (Met1as) within the endosperm. Crosses between two 2xMet1as plants result in seed with a slightly increased number of endosperm nuclei and normal seed weight (Table 1), which is most easily explained by proposing that the combination of hypomethylated gametes of both sexes allows normal endosperm development.

(Emphasis added)

Example 3 in the specification discusses the construction of a Met1 antisense construct which uses an AGL5 promoter, which is described as a female germ line specific promoter. The AGL5 gene is discussed in Savidge, et al., The Plant Cell 7:721-733 (1995), where it is stated that AGL5 is expressed in an organ-specific manner. Savidge et al. at page 731, right-hand column. A copy of this reference is included in the attached IDS.

In view of the specification as a whole and the paragraphs above in particular, the expression pattern of the AGL5 promoter is suitably described as targeting the female germ line, whereas the expression pattern of a CaMV35S promoter cannot be described as targeting the female germ line. The purpose behind use of a promoter targeting the femal germ line is that expression in female germ line cells prevents abnormalities associated with expression with a CaMV35S driven MET1 antisense gene. Nowhere in Ronemus *et al.* is there any mention of expression targeted to female germ line cells, nor any hint that there would have been a desirable purpose for such targeting. Thus, Ronemus *et al.* does not teach all the elements of the claimed method.

The Examiner is requested to withdraw the rejection of claims 20-21, 62-67, 69, 71, 76-78 and 80-82 under 35 U.S.C. §102(b).

CONCLUSION

In view of the remarks above, Applicant respectfully requests entry of the amendments above and earnestly solicits favorable consideration and allowance of the pending claims. The Examiner is invited to telephone the undersigned if it is felt that such would expedite prosecution.

Enclosed is a check for $225.00 check for the Petition for Extension of Time fee. Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: Nov 7, 2005

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